

Amendments to the Specification:

Please replace the fourth paragraph on page 23 of the application as filed, by the following paragraph:

Such homology determinations may be made using oligonucleotide alignment algorithms for example, but not limited to a BLAST (using default parameters: program: blastn; Database: nr; Expect10; filter: default; Alignment: pairwise; Query genetic Codes: Standard (1) or FASTA, again using default parameters. Using sequence similarity searches *AtBBM* exhibits about 85% homology with the full length of *BNM3*, and therefore, *AtBBM* is a *BNM3* gene. Furthermore, a *BNM3* gene may also be defined in terms of its ability to hybridize with sequences disclosed in the present invention. Therefore, “*BNM3*” or “*BNM3* gene”, also includes: